



Supplementary Fig. S3: Effect of therapy on CD4⁺ and CD8⁺ T cells infiltrating ID8 tumors.

(A) Frequency of T-cell subsets by scRNAseq; precursor exhausted (Tpex), terminal exhausted (Tex), effector memory (EM), T helper 1 (Th1), T follicular helper (Tfh), regulatory T cell (Treg), and naïve like T cells in all three control tumors vs individual tumors (#1-3) from CIM or RACIM. Table describes CD8 and CD4:Treg ratios. **(B)** Bar plots representing the most clonally expanded CD4⁺ T-cell clonotypes (by TCRseq) following RACIM (TCRs of all 3 tumors are shown in #1, vs. in individual tumors in #2-4). **(C)** Pseudotime trajectory analysis of CD4 clusters (as in Fig. 4F) showing the trajectory and gradual up/downregulation of indicated genes. **(D-E)** Immune cell phenotypes were evaluated on single cell suspensions of ID8 tumors treated with LD-WART, CIM or RACIM and control ID8 tumors. **(D)** Representative flow cytometry bar plot and gating strategy of TCF1^{-/+}PD1^{+/-} CD4⁺ TILs. **(E)** Flow cytometric evaluation of co-expression of indicated inhibitory receptors on TCF1⁻PD1⁺CD4⁺ TILs. **(F)** Histogram representing flow cytometry evaluation of cell-surface coexpression of indicated costimulatory receptors by TCF1⁻PD1⁺CD4⁺ cells. **(G)** Flow cytometry evaluation TCF1^{-/+}PD1^{+/-} CD8⁺ TIL subsets and representative gating strategy. **(H)** Histogram depicting co-expression of indicated co-inhibitory receptors on CD8⁺ TCF1⁻PD1⁺ TILs as evaluated by flow cytometry analysis. **(I)** Histogram depicting coexpression of indicated costimulatory receptors on CD8⁺TCF1⁻PD1⁺ TILs as evaluated by flow cytometric analysis. Data are representative of 2 to 3 independent experiments with n=5 mice per group. Statistical analysis was performed using Student's unpaired *t*-test or Kruskal Wallis for multiple comparisons, error bars represent mean ± standard deviation. **P* ≤ 0.05, ***P* < 0.01, ****P* < 0.001, *****P* < 0.0001.